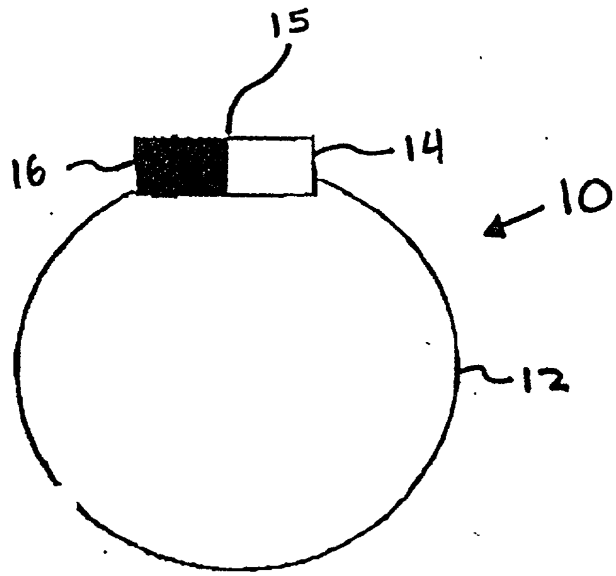

FIG. 1A

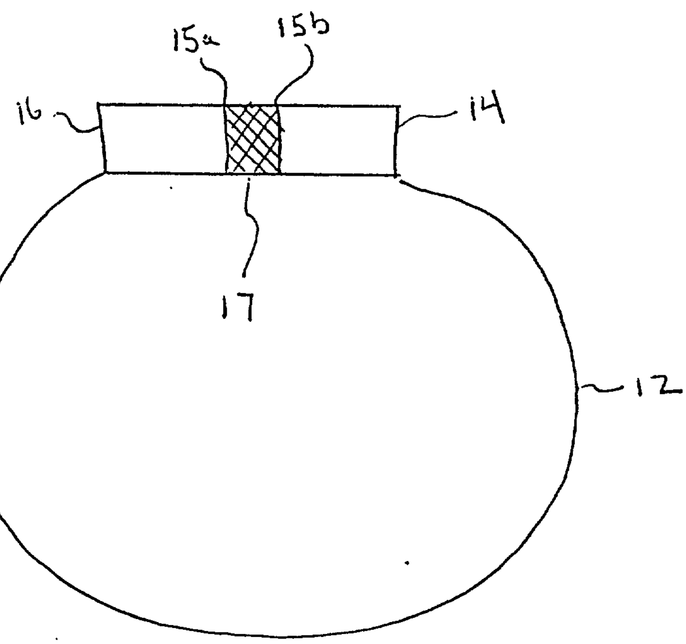

FIG. 1B

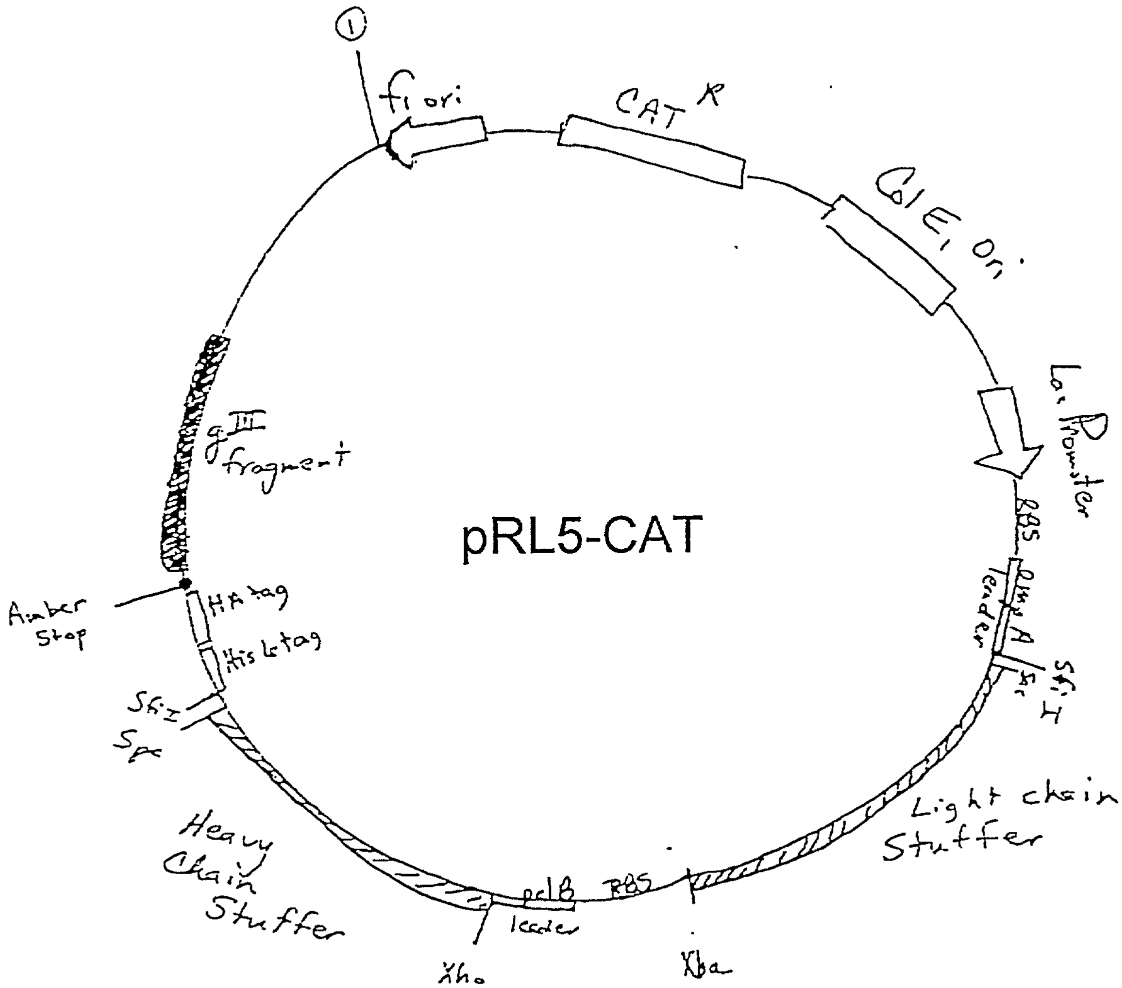
1
f1 ori
CAT R
ColE1 ori
Lac Promoter
RBS
OmpA leader
Sfi I
Light chain Stuffer
Xba
RBS
pelB leader
Xho
Heavy Chain Stuffer
Sfi I
His6 tag
HA tag
Amber Stop
gIII fragment
pRL5-CAT

FIG. 2

PRL5-CAT

5'GGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTA
AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAAT
CAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAG
TCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTAT
CAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTC
GAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGA
GCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGC
GAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGT
AACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGC
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACA
TTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAAT
ATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCC
TTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAA
GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGG
ATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCA
ATGATGAGCACTTTTCGACCGAATAAATACCTGTGACGGAAGATCACTTCGC
AGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAAC
TTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACC
ATAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTGTCGAGATTTTCA
GGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTT
GATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGC
TCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGA
CCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCC
CGCCTGATGAATGCTCATCCGGAATTACGTATGGCAATGAAAGACGGTGAGC
TGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAACT
GAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCT
ACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCC
CTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGT
TTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGT
TTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTG
GCGATTCAGGTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCAGAATGCT
TAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTT
TAAGGCAGTTATTGGTGCCCTTAAACGCCTGGTTGCTACGCCTGAATAAGTGA
TAATAAGCGGATGAATGGCAGAAATTCGAAAGCAAATTCGACCCGGTCGTCG
GTTCAGGGCAGGGTCGTTAAATAGCCGCTTATGTCTATTGCTGGTTTACCGGT
TTATTGACTACCGGAAGCAGTGTGACCGTGTGCTTCTCAAATGCCTGAGGCCA
GTTTGCTCAGGCTCTCCCCGTGGAGGTAATAATTGACGATATGATCCTTTTTT
TCTGATCAAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAA
ATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGAT
CAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAA
CAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACC
AACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACT
GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACC
GCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCG

FIG. 3A

ATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGC
GCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGA
ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCA
CGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCG
GAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTT
ATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGC
TCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTAC
GGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCC
CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGC
CGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG
CGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCA
GCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAAT
TAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTC
CGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTGAATTCAGGAGG
AATTTAAAATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTT
CGCTACCGTGGCCCAGGCGGCCGAGCTCGACTGCACTGGATGGTGGCGCTGG
ATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGTCGCTCCACAAGG
TAAACAGTTGATTGAACTGCCTGAACTACCGCAGCCGGAGAGCGCCGGGCAA
CTCTGGCTCACAGTACGCGTAGTGCAACCGAACGCGACCGCATGGTCAGAAG
CCGGGCACATCAGCGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGT
GACGCTCCCCGCCGCGTCCCACGCCATCCCGCATCTGACCACCAGCGAAATG
GATTTTTGCATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAG
GCTTTCTTTCACAGATGTGGATTGGCGATAAAAAACAACTGCTGACGCCGCT
GCGCGATCAGTTCACCCGTGCACCGCTGGATAACGACATTGGCGTAAGTGAA
GCGACCCGCATTGACCCTAACGCCTGGGTCGAACGCTGGAAGGCGGCGGGCC
ATTACCAGGCCGAAGCAGCGTTGTTGCAGTGCACGGCAGATACACTTGCTGA
TGCGGTGCTGATTACGACCGCTCACGCGTGGCAGCATCAGGGGAAAACCTTA
TTTATCAGCCGGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCGATTA
CCGTTGATGTTGAAGTGGCGAGCGATACACCGCATCCGGCGCGGATTGGCCT
GAACTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAAACTGGCTCGGATTAGG
GCCGCAAGAAAACTATCCCGACCGCCTTACTGCCGCCTGTTTTGACCGCTGGG
ATCTGCCATTGTCAGACATGTATACTGGCTGCACCATCTGTCTTCATCTTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAG
CACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA
CACAAAGTATATGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCA
CAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGA
ATTTAAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCG
CTGCCCAACCAGCCATGGCCCTCGAGCTGATGAGCCATGGAAGCTGTGTCGC
CTGCACCAGGCTCCCACGGCTCGTGGTGCGGTGCGCTTCTGGTGTTCGCTGCC
TACAGCCGACACGTCGAGCTTCGTGCCCCTAGAGTTGCGCGTCACAGCAGCC
TCCGGCGCTCCGCGATATCACCGTGTCATCCACATCAATGAAGTAGTGCTCCT
AGACGCCCCCGTGGGGCTGGTGGCGCGGTTGGCTGACGAGAGCGGCCACGTA
GTGTTGCGCTGGCTCCCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTA
CGAGGTGGACGTCTCGGCCGGCAACGGCGCAGGGAGCGTACAGAGGGTGGA

FIG. 3B

GATCCTGGAGGGCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCCGGACG
CGCTACACCTTCGCCGTCCGCGCGTATGGCTGAGCCGAGCTTCGGCGGCTT
CTGGAGCGCCTGGTCGGAGCCTGTGTCGCTGCTGACGCCTAGCGACCTGGAC
CCCCTCATCCTGACGCTCTCCCTCATCCTCGTGGTCATCCTGGTGCTGCTGAC
CGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAGCAGAAGATCTGGCCT
GGCATCCCGAGCCCAGAGAGCGAGTTTGAAGGCCTCTTCACCACCCACAAGG
GTAACTTCCAGCTGTGGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCCC
CTGCACCCCCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGC
GCTGCTGGGGGACGATGCAGGCAGTGGAGCCGGGGACAGATGATGAGGGCC
CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG
TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTAGTGGCCAG
GCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGG
ACTACGCTTCTTAGGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGG
CGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATT
ATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATG
AAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTGTCGCTACTGA
TTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATG
GTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTC
GGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTC
CCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTAGCGCTGGTAAACCAT
ATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCG
TTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACATA
CTGCGTAATAAGGAGTCTTAAGCTAGCTAATTAATTTAAGCGGCCGCAGATC
T 3'

FIG. 3C

(Seq. ID No. 1)

```
                         Ssp I
GGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGC   59
CCCTTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCG
```

(Seq ID No. 2)

```
                                           Psi I
TCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGAC   118
AGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTG

CGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGG   177
GCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACC

                                                  Ade I
     Drd I                                        Dra III
ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCA   236
TGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGT

TCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA   295
AGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATT

                                    NgoM IV
                                     Nae I
AGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAG   354
TCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTC

                 BsrB I
                 Mbi I
GGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGC   413
CCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCG
```

Fig. 4A

GTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTT 472
CATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAA

TCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGT 531
AGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACA

BsrB I
Mbi I
BspH I
Bci VI
Ssp I
Ear I

ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT 590
TAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCA

ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCC 649
TACTCATAAGTTGTAAAGGCACAGCGGGAATAAGGGAAAAAACGCCGTAAAACGGAAGG
Amp frag

Alw44 I
ApaL I

TGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTG 708
ACAAAAACGAGTGGGTCTTTGCGACCACTTTCATTTTCTACGACTTCTAGTCAACCCAC
Amp frag

BssS I
Eco57 I

CACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGC 767
GTGCTCACCCAATGTAGCTTGACCTAGAGTTGTCGCCATTCTAGGAACTCTCAAAAGCG
Amp frag

Fig. 4B

```
   Aci II
   Xmn I
CCCGAAGAACGTTTTCCAATGATGAGCACTTTTCGACCGAATAAATACCTGTGACGGAA  826
GGGCTTCTTGCAAAAGGTTACTACTCGTGAAAAGCTGGCTTATTTATGGACACTGCCTT
          Amp frag

GATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGC  885
CTAGTGAAGCGTCTTATTTATTTAGGACCACAGGGACAACTATGGCCCTTCGGGACCCG

           BsmB I
   Van91 I Esp3 I
CAACTTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACCATA  944
GTTGAAAACCGCTTTTACTCTGCAACTAGCCGTGCATTCTCCAAGGTTGAAAGTGGTAT

                                                      Bpu10 I
ATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTGTCGAGATTTTCAGGAGCTAAG  1003
TACTTTATTCTAGTGATGGCCCGCATAAAAAACTCAACAGCTCTAAAGTCCTCGATTC

GAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCA  1062
CTTCGATTTTACCTCTTTTTTTAGTGACCTATATGGTGGCAACTATATAGGGTTACCGT
         Chloramphenicol transferase

TCGTAAAGAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCG  1121
AGCATTTCTTGTAAAACTCCGTAAAGTCAGTCAACGAGTTACATGGATATTGGTCTGGC
         Chloramphenicol transferase
```

Fig. 4C

472

Pvu II   Dra I

TTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTAT 1180

AAGTCGACCTATAATGCCGGAAAAATTTCTGGCATTTCTTTTTATTCGTGTTCAAAATA

Chloramphenicol transferase

BsaM I   Acc III   SnaB I

CCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTACGTATGGC 1239

GGCCGGAAATAAGTGTAAGAACGGGCGGACTACTTACGAGTAGGCCTTAATGCATACCG

Chloramphenicol transferase

BseM I
BsrD I

AATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCC 1298

TTACTTTCTGCCACTCGACCACTATACCCTATCACAAGTGGGAACAATGTGGCAAAAGG

Chloramphenicol transferase

Aci II   Bpm I

ATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAG 1357

TACTCGTTTGACTTTGCAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAGGCCGTC

Chloramphenicol transferase

TTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCC 1416

AAAGATGTGTATATAAGCGTTCTACACCGCACAATGCCACTTTTGGACCGGATAAAGGG

Chloramphenicol transferase

Fig. 4D

472

```
                                          BsmB I
                                          Esp3 I     Van91 I
TAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCA  1475
ATTTCCCAAATAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGT
                 Chloramphenicol transferase

                   Bal I                                Bsp19 I
          Dra I    Msc I                                Nco I
GTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGC  1534
CAAAACTAAATTTGCACCGGTTATACCTGTTGAAGAAGCGGGGGCAAAAGTGGTACCCG
                 Chloramphenicol transferase

    Ssp I
AAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGC  1593
TTTATAATATGCGTTCCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACG
                 Chloramphenicol transferase

                                        BsaM I           Sca I
CGTTTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATG  1652
GCAAACACTACCGAAGGTACAGCCGTCTTACGAATTACTTAATGTTGTCATGACGCTAC
                 Chloramphenicol transferase

AGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCTTAAACGCCTGGT  1711
TCACCGTCCCGCCCCGCATTAAAAAAATTCCGTCAATAACCACGGGAATTTGCGGACCA
```

Fig. 4E

BstB1
Csp45 I

TGCTACGCCTGAATAAGTGATAATAAGCGGATGAATGGCAGAAATTCGAAAGCAAATTC 1770
ACGATGCGGACTTATTCACTATTATTCGCCTACTTACCGTCTTTAAGCTTTCGTTTAAG

Tth111 I
Drd I

GACCCGGTCGTCGGTTCAGGGCAGGGTCGTTAAATAGCCGCTTATGTCTATTGCTGGTT 1829
CTGGGCCAGCAGCCAAGTCCCGTCCCAGCAATTTATCGGCGAATACAGATAACGACCAA

Age I
PinA I
Bsu36 I

TACCGGTTTATTGACTACCGGAAGCAGTGTGACCGTGTGCTTCTCAAATGCCTGAGGCC 1888
ATGGCCAAATAACTGATGGCCTTCGTCACACTGGCACACGAAGAGTTTACGGACTCCGG

Bpu10 I
Bcl I

AGTTTGCTCAGGCTCTCCCCGTGGAGGTAATAATTGACGATATGATCCTTTTTTTCTGA 1947
TCAAACGAGTCCGAGAGGGGCACCTCCATTATTAACTGCTATACTAGGAAAAAAAGACT

BspH I

TCAAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACG 2006
AGTTTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGC

TGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 2065
ACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTC

ori

ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCG 2124
TAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGC

ori

Fig. 4F

Eco57 I

GTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAG 2183
CACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTC
ori

CAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCA 2242
GTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGT
ori

AlwN I

AGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCT 2301
TCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGA
ori

GCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA 2360
CGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATT
ori

Alw44 I
ApaL I

GGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGA 2419
CCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCT
ori

CCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAA 2478
GGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTT
ori

Fig. 4G

Bci VI — BssS I

GGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAG 2537
CCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTC
ori

GGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCT 2596
CCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGA
ori

Drd I

GACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCC 2655
CTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGG
ori

BspLU11 I

AGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTT 2714
TCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAA

TCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATA 2773
AGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGAAACTCACTCGACTAT

BsrB I — Ear I
Mbi I — Sap I

CCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG 2832
GGCGAGCGGCGTCGGCTTGCTGGCTCGCGTCGCTCAGTCACTCGCTCCTTCGCCTTCTC

Fig. 4H

472

Ase I
Vsp I
Pvu II

```
CGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCA  2891
GCGGGTTATGCGTTTGGCGGAGAGGGGCGCGCAACCGGCTAAGTAATTACGTCGACCGT
```

lac promoter

Ase I
Vsp I

```
CGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGC  2950
GCTGTCCAAAGGGCTGACCTTTCGCCCGTCACTCGCGTTGCGTTAATTACACTCAATCG
```

lac promoter

```
TCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGA  3009
AGTGAGTAATCCGTGGGGTCCGAAATGTGAAATACGAAGGCCGAGCATACAACACACCT
```

lac promoter

BsrB I
Mbi I
Mfe I
Mun I
EcoR I
Dra I
Nru I

```
ATTGTGAGCGGATAACAATTGAATTCAGGAGGAATTTAAAATGAAAAAGACAGCTATCG  3068
TAACACTCGCCTATTGTTAACTTAAGTCCTCCTTAAATTTTACTTTTTCTGTCGATAGC
```

lac promoter
Omp A leader
mRNA start
rbs
lac rep site

Fig. 4I

Bsg I
Bgl I
Sfi I
Eco52 I
Xma III
EcoICR I
Sac I
Sst I

CGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAGGCGGCCGAGCTCGACTGC 3127
GCTAACGTCACCGTGACCGACCAAAGCGATGGCACCGGGTCCGCCGGCTCGAGCTGACG

Omp A leader

n-omp

Omp A cleavage

ACTGGATGGTGGCGCTGGATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGTC 3186
TGACCTACCACCGCGACCTACCATTCGGCGACCGTTCGCCACTTCACGGAGACCTACAG

LCV stuffer

GCTCCACAAGGTAAACAGTTGATTGAACTGCCTGAACTACCGCAGCCGGAGAGCGCCGG 3245
CGAGGTGTTCCATTTGTCAACTAACTTGACGGACTTGATGGCGTCGGCCTCTCGCGGCC

LCV stuffer

Mlu I
Drd I

GCAACTCTGGCTCACAGTACGCGTAGTGCAACCGAACGCGACCGCATGGTCAGAAGCCG 3304
CGTTGAGACCGAGTGTCATGCGCATCACGTTGGCTTGCGCTGGCGTACCAGTCTTCGGC

LCV stuffer

AlwN I

GGCACATCAGCGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGTGACGCTCCCC 3363
CCGTGTAGTCGCGGACCGTCGTCACCGCAGACCGCCTTTTGGAGTCACACTGCGAGGGG

LCV stuffer

Fig. 4J

```
                                                         Xcm I
                                                              BstX I
GCCGCGTCCCACGCCATCCCGCATCTGACCACCAGCGAAATGGATTTTTGCATCGAGCT
                                                                   3422
CGGCGCAGGGTGCGGTAGGGCGTAGACTGGTGGTCGCTTTACCTAAAAACGTAGCTCGA
                            LCV stuffer

                                                 Bgl I
GGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAGGCTTTCTTTCACAGATGTGGATTG
                                                                   3481
CCCATTATTCGCAACCGTTAAATTGGCGGTCAGTCCGAAAGAAAGTGTCTACACCTAAC
                            LCV stuffer

                                                         Alw44 I
                                                         ApaL I
GCGATAAAAAACAACTGCTGACGCCGCTGCGCGATCAGTTCACCCGTGCACCGCTGGAT
                                                                   3540
CGCTATTTTTTGTTGACGACTGCGGCGACGCGCTAGTCAAGTGGGCACGTGGCGACCTA
                            LCV stuffer

AACGACATTGGCGTAAGTGAAGCGACCCGCATTGACCCTAACGCCTGGGTCGAACGCTG
                                                                   3599
TTGCTGTAACCGCATTCACTTCGCTGGGCGTAACTGGGATTGCGGACCCAGCTTGCGAC
                            LCV stuffer

                                                     Alw44 I
                                                     ApaL I
GAAGGCGGCGGGCCATTACCAGGCCGAAGCAGCGTTGTTGCAGTGCACGGCAGATACAC
                                                                   3658
CTTCCGCCGCCCGGTAATGGTCCGGCTTCGTCGCAACAACGTCACGTGCCGTCTATGTG
                            LCV stuffer
```

Fig. 4K

BsrB I
Mbi I Mlu I

TTGCTGATGCGGTGCTGATTACGACCGCTCACGCGTGGCAGCATCAGGGGAAAACCTTA 3717
AACGACTACGCCACGACTAATGCTGGCGAGTGCGCACCGTCGTAGTCCCCTTTTGGAAT
LCV stuffer

TTTATCAGCCGGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCGATTACCGTTGA 3776
AAATAGTCGGCCTTTTGGATGGCCTAACTACCATCACCAGTTTACCGCTAATGGCAACT
LCV stuffer

BspM I
Pvu II

TGTTGAAGTGGCGAGCGATACACCGCATCCGGCGCGGATTGGCCTGAACTGCCAGCTGG 3835
ACAACTTCACCGCTCGCTATGTGGCGTAGGCCGCGCCTAACCGGACTTGACGGTCGACC
LCV stuffer

BsrB I
Mbi I

CGCAGGTAGCAGAGCGGGTAAACTGGCTCGGATTAGGGCCGCAAGAAAACTATCCCGAC 3894
GCGTCCATCGTCTCGCCCATTTGACCGAGCCTAATCCCGGCGTTCTTTTGATAGGGCTG
LCV stuffer

Bsg I
BspLU11 I
Acc I
Bst1107 I

CGCCTTACTGCCGCCTGTTTTGACCGCTGGGATCTGCCATTGTCAGACATGTATACTGG 3953
GCGGAATGACGGCGGACAAAACTGGCGACCCTAGACGGTAACAGTCTGTACATATGACC
LCV stuffer

001013mw2
001013mw1

Fig. 4L

Bbs I

```
CTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCC  4012
GACGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGG
```

Kappa Cns

001013mw1

Xmn I

```
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGT  4071
AGACAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCA
```

Kappa Cns

```
GGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGG  4130
CCTATTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCC
```

Kappa Cns

BbvC I
Bpu10 I

```
ACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACAC  4189
TGTCGTGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTG
```

Kappa Cns

AlwN I
Bpu10 I

```
AAAGTATATGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTT  4248
TTTCATATACGGACGCTTCAGTGGGTAGTCCCGGACTCGAACGGGCAGTGTTTCTCGAA
```

Kappa Cns

Fig. 4M

```
                                  Ase I
                        Xba I     Vsp I              Dra I
CAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACC  4307
GTTGTCCCCTCTCACAATCAAGATCTATTAATTAATCCTCCTTAAATTTTACTTTATGG
------ Kappa Cns ------                            pel B leader
```

```
                                                      Bsp19 I
                   AlwN I                             Nco I    Xho I
TATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCCTC  4366
ATAACGGATGCCGTCGGCGACCTAACAATAATGAGCGACGGGTTGGTCGGTACCGGGAG
------------------------ pel B leader ---------------------
                                         <---- Lead B ----
                                         ---- Lead VH ---->
```

```
           Bsp19 I
           Nco I
                Bsg I               EcoN I              BssS I
GAGCTGATGAGCCATGGAAGCTGTGTCGCCTGCACCAGGCTCCCACGGCTCGTGGTGCG  4425
CTCGACTACTCGGTACCTTCGACACAGCGGACGTGGTCCGAGGGTGCCGAGCACCACGC
                         HCV stf
```

```
                                          Btr I
GTGCGCTTCTGGTGTTCGCTGCCTACAGCCGACACGTCGAGCTTCGTGCCCCTAGAGTT  4484
CACGCGAAGACCACAAGCGACGGATGTCGGCTGTGCAGCTCGAAGCACGGGGATCTCAA
                         HCV stf
```

```
 Bcg I                                   EcoR V
GCGCGTCACAGCAGCCTCCGGCGCTCCGCGATATCACCGTGTCATCCACATCAATGAAG  4543
CGCGCAGTGTCGTCGGAGGCCGCGAGGCGCTATAGTGGCACAGTAGGTGTAGTTACTTC
                         HCV stf
```

Fig. 4N

BsrB I
Mbi I

```
TAGTGCTCCTAGACGCCCCCGTGGGGCTGGTGGCGCGGTTGGCTGACGAGAGCGGCCAC
                                                              4602
ATCACGAGGATCTGCGGGGGCACCCCGACCACCGCGCCAACCGACTGCTCTCGCCGGTG
```

HCV stf

Ade I
Dra III
Aat II
BsmB I
Esp3 I

```
GTAGTGTTGCGCTGGCTCCCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTACGA
                                                              4661
CATCACAACGCGACCGAGGGCGGCGGACTCTGTGGGTACTGCAGAGTGTAGGCGATGCT
```

HCV stf

Aat II
Eco52 I
Xma III
BsmB I
Esp3 I
NgoM IV
Nae I

```
GGTGGACGTCTCGGCCGGCAACGGCGCAGGGAGCGTACAGAGGGTGGAGATCCTGGAGG
                                                              4720
CCACCTGCAGAGCCGGCCGTTGCCGCGTCCCTCGCATGTCTCCCACCTCTAGGACCTCC
```

HCV stf

Ade I
Dra III
Bpm I
BspM I

```
GCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCCGGACGCGCTACACCTTCGCCGTC
                                                              4779
CGGCGTGGCTCACACACGACTCGTTGGACGCCCCGGCCTGCGCGATGTGGAAGCGGCAG
```

HCV stf

BssH II
Bpm I

```
CGCGCGCGTATGGCTGAGCCGAGCTTCGGCGGCTTCTGGAGCGCCTGGTCGGAGCCTGT
                                                              4838
GCGCGCGCATACCGACTCGGCTCGAAGCCGCCGAAGACCTCGCGGACCAGCCTCGGACA
```

HCV stf

Fig. 4O

BssS I

GTCGCTGCTGACGCCTAGCGACCTGGACCCCCTCATCCTGACGCTCTCCCTCATCCTCG 4897
CAGCGACGACTGCGGATCGCTGGACCTGGGGGAGTAGGACTGCGAGAGGGAGTAGGAGC
HCV stf

TGGTCATCCTGGTGCTGCTGACCGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAG 4956
ACCAGTAGGACCACGACGACTGGCACGAGCGCGACGAGAGGGTGGCGGCCCGAGACTTC
HCV stf

Bgl II Eco57 I Stu I Ear I

CAGAAGATCTGGCCTGGCATCCCGAGCCCAGAGAGCGAGTTTGAAGGCCTCTTCACCAC 5015
GTCTTCTAGACCGGACCGTAGGGCTCGGGTCTCTCGCTCAAACTTCCGGAGAAGTGGTG
HCV stf

Pvu II BstX I Bsg I

CCACAAGGGTAACTTCCAGCTGTGGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCC 5074
GGTGTTCCCATTGAAGGTCGACACCGACATGGTCTTACTACCGACGGACACCACCTCGG
HCV stf

BspM I Eco47 III

CCTGCACCCCCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGCGCTGC 5133
GGACGTGGGGGAAGTGCCTCCTGGGTGGACGAAGGGACCTTCAGGAGAGTCTCGCGACG
HCV stf

PspOM I
Bbs I
Apa I

TGGGGGACGATGCAGGCAGTGGAGCCGGGGACAGATGATGAGGGCCCATCGGTCTTCCC 5192
ACCCCCTGCTACGTCCGTCACCTCGGCCCCTGTCTACTACTCCCGGGTAGCCAGAAGGG
HCV stf

Fig. 4P

BseR I, EcoN I

```
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA 5251
GGACCGTGGGAGGAGGTTCTCGTGGAGACCCCCGTGTCGCCGGGACCCGACGGACCAGT
```

Age I, PinA I, Tth111 I, Kas I, Nar I, Ehe I, Bbe I

```
AGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGC 5310
TCCTGATGAAGGGGCTTGGCCACTGCCACAGCACCTTGAGTCCGCGGGACTGGTCGCCG
```

Alw44 I, ApaL I, Bsu36 I, BbvC I, Bpu10 I, Bpm I, BstE II

```
GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT 5369
CACGTGTGGAAGGGCCGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTCGCACCA
```

BstX I

```
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC 5428
CTGGCACGGGAGGTCGTCGAACCCGTGGGTCTGGATGTAGACGTTGCACTTAGTGTTCG
```

Bcu I, Spe I, Bcu I, Bal I, Msc I

```
CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTAGTGGC 5487
GGTCGTTGTGGTTCCACCTGTTCTTTCAACTCGGGTTTAGAACACTGTTTTGATCACCG
```

Fig. 4Q

NgoM IV
Bgl I
Sfi I
Nae I
Fse I
Bsp19 I
Nco I
BstX I
BsiW I
Acc III

CAGGCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTA 5546
GTCCGGCCGGTCGTGGTAGTGGTAGTGGTACCGCGTATGGGCATGCTGCAAGGCCTGAT

linker — His tag — HA tag

CGCTTCTTAGGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGG 5605
GCGAAGAATCCTCCCACCACCGAGACTCCCACCGCCAAGACTCCCACCGCCGAGACTCC

HA tag — st — gene III

GAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAAAC 5664
CTCCGCCAAGGCCACCACCGAGACCAAGGCCACTAAAACTAATACTTTTCTACCGTTTG

gene III

GCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAGTCTGACGCTAA 5723
CGATTATTCCCCCGATACTGGCTTTTACGGCTACTTTTGCGCGATGTCAGACTGCGATT

gene III

BspD I
Cla I

AGGCAAACTTGATTCTGTCGCTACTGATTACGGTGCTGCTATCGATGGTTTCATTGGTG 5782
TCCGTTTGAACTAAGACAGCGATGACTAATGCCACGACGATAGCTACCAAAGTAACCAC

gene III

Fig. 4R

472

```
ACGTTTCCGGCCTTGCTAATGGTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCC
                                                            5841
TGCAAAGGCCGGAACGATTACCATTACCACGATGACCACTAAAACGACCGAGATTAAGG
---------------------------- gene III ---------------------------

                                             Xmn I       Ssp I
CAAATGGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATA
                                                            5900
GTTTACCGAGTTCAGCCACTGCCACTATTAAGTGGAAATTACTTATTAAAGGCAGTTAT
---------------------------- gene III ---------------------------

                                                Eco47 III
TTTACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTAGCGCTGGTAAAC
                                                            5959
AAATGGAAGGGAGGGAGTTAGCCAACTTACAGCGGGAAAACAGAAATCGCGACCATTTG
---------------------------- gene III ---------------------------

  Nde I
CATATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCGTTT
                                                            6018
GTATACTTAAAAGATAACTAACACTGTTTTATTTGAATAAGGCACCACAGAAACGCAAA
---------------------------- gene III ---------------------------

CTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACATACTGCGTAA
                                                            6077
GAAAATATACAACGGTGGAAATACATACATAAAAGATGCAAACGATTGTATGACGCATT
---------------------------- gene III ---------------------------
      <------- 991222nw3 -------
```

Fig. 4S

CciN I
Eco52 I
Bst98 I Ase I Not I
Nhe I Vsp I Xma III Bgl II

```
TAAGGAGTCTTAAGCTAGCTAATTAATTTAAGCGGCCGCAGATCT  6122
ATTCCTCAGAATTCGATCGATTAATTAAATTCGCCGGCGTCTAGA
```

—— gene III ——

Fig. 4T

472

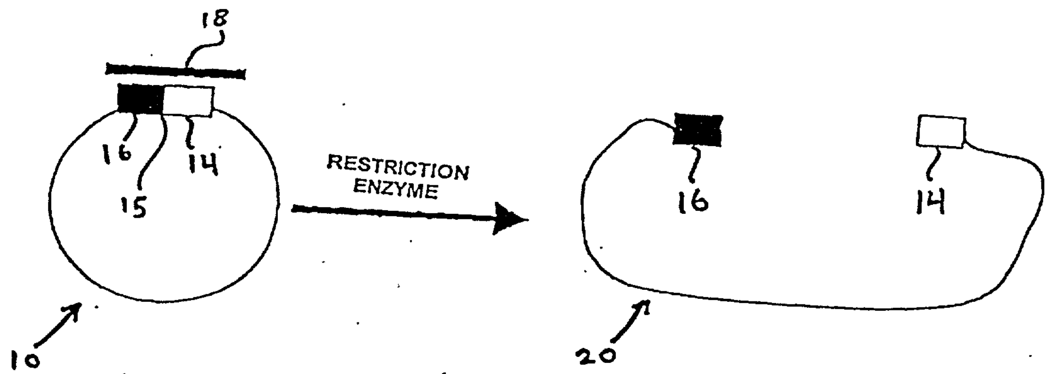

FIG. 5A

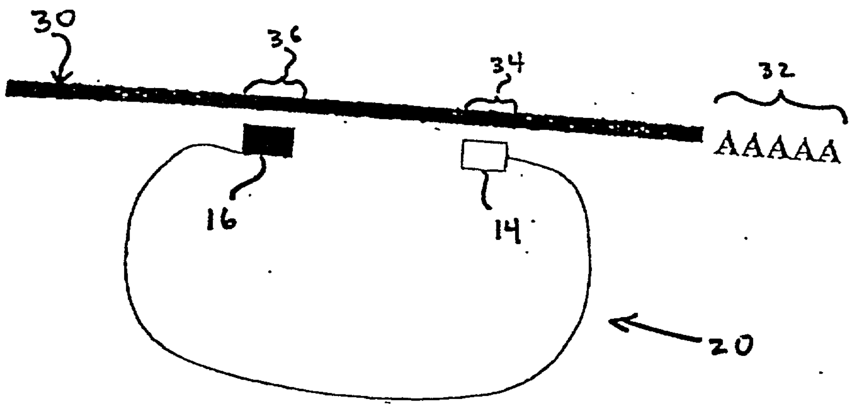

FIG. 5B

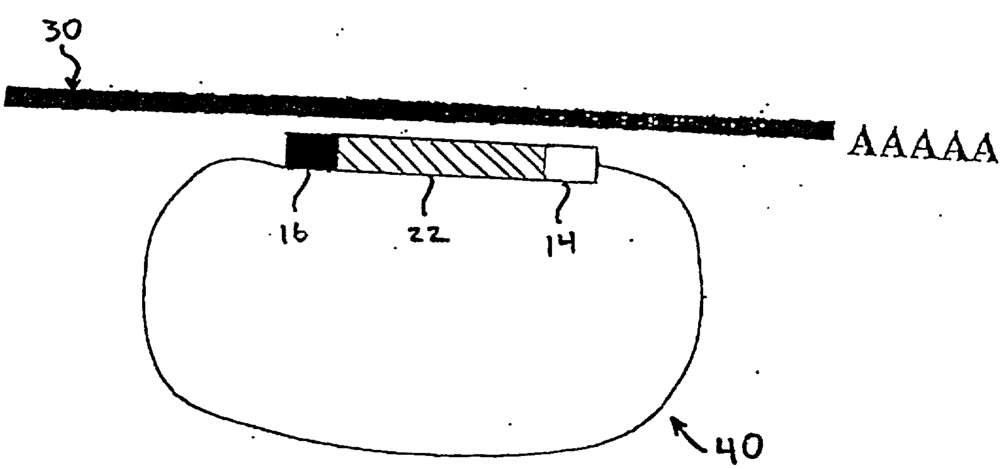

FIG. 5C

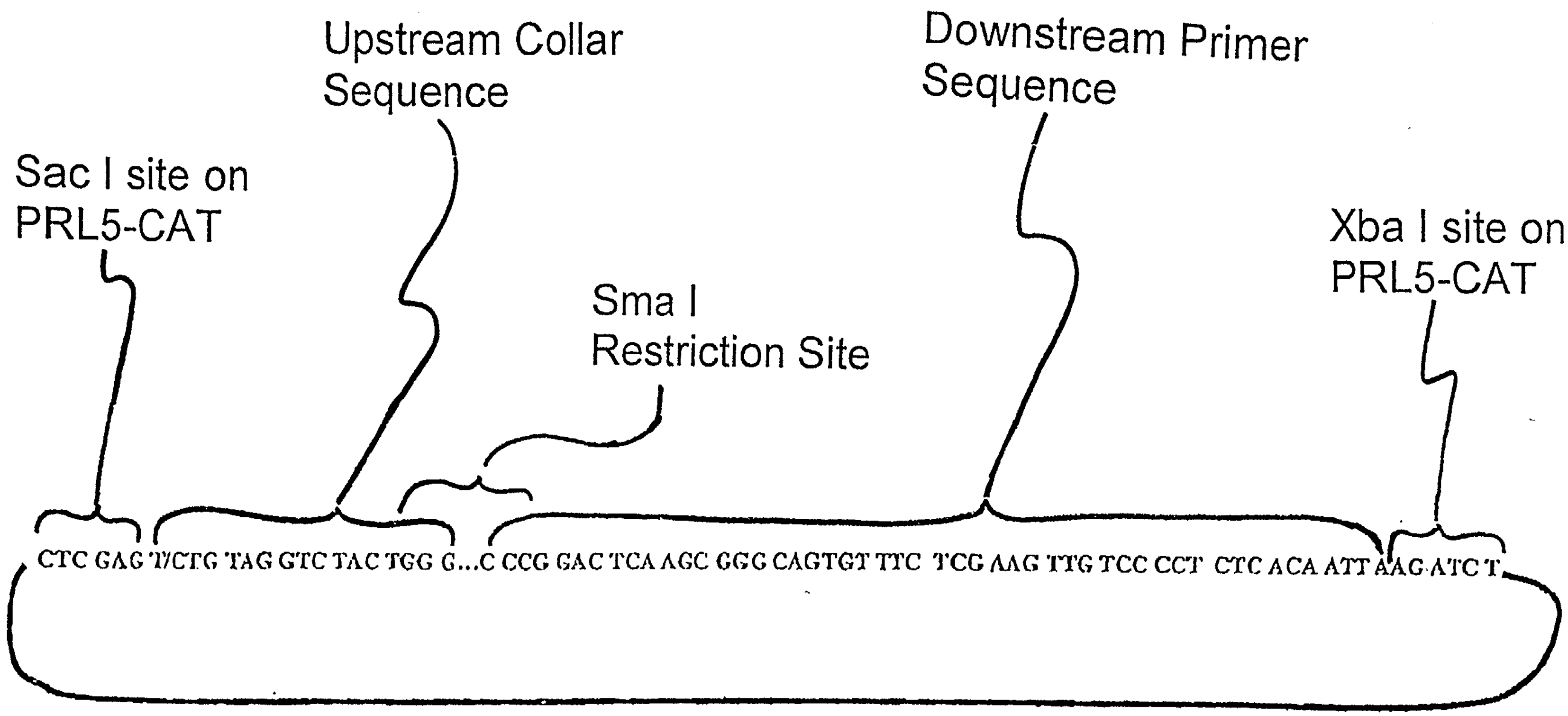
Sac I site on PRL5-CAT
Upstream Collar Sequence
Sma I Restriction Site
Downstream Primer Sequence
Xba I site on PRL5-CAT
CTC GAG T/CTG TAG GTC TAC TGG G...C CCG GAC TCA AGC GGG CAGTGT TTC TCG AAG TTG TCC CCT CTC ACA ATT AAG ATC T

FIG. 6A

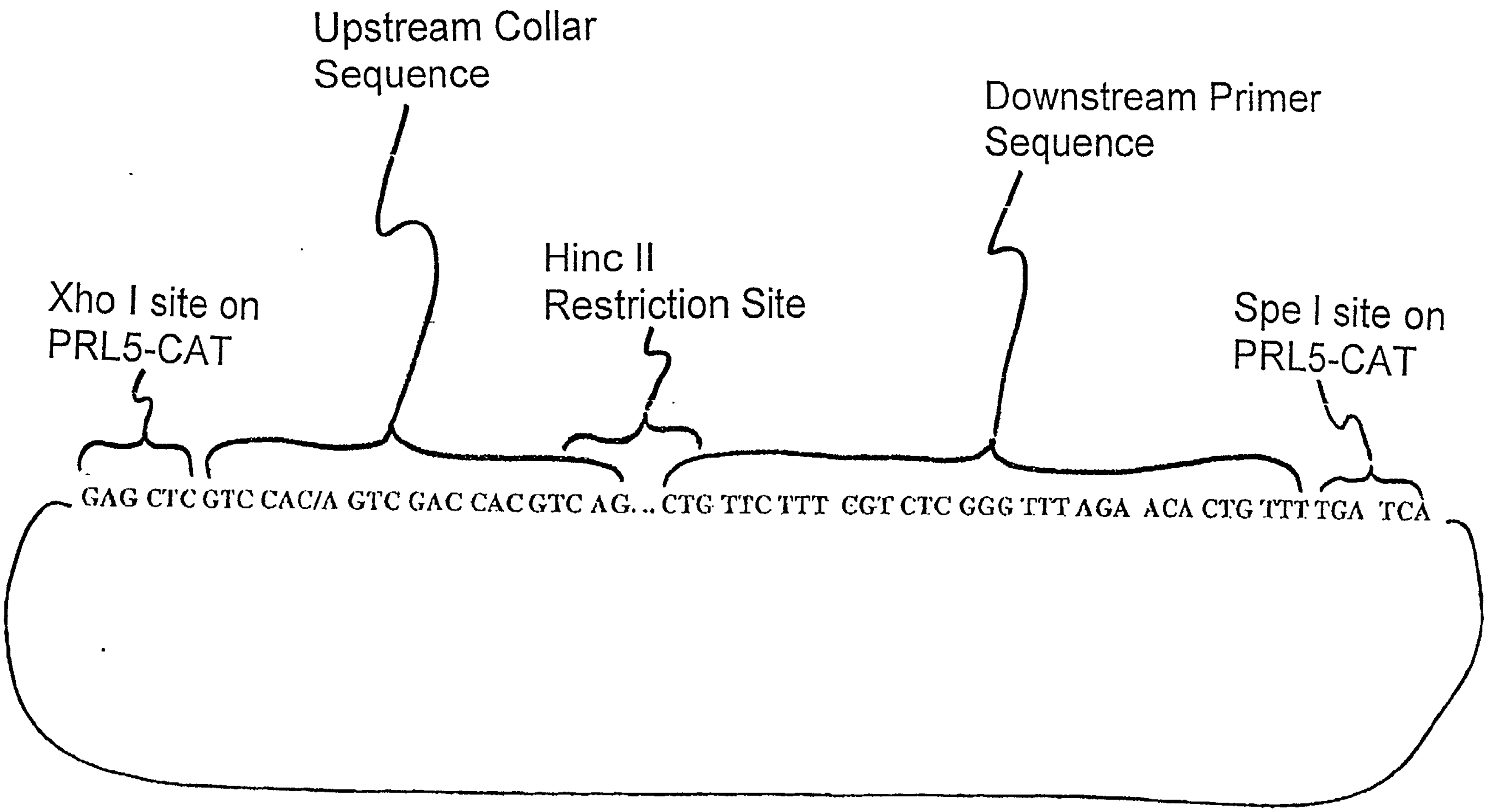
Upstream Collar
Sequence
Downstream Primer
Sequence
Hinc II
Restriction Site
Xho I site on
PRL5-CAT
Spe I site on
PRL5-CAT
GAG CTC GTC CAC/A GTC GAC CAC GTC AG... CTG TTC TTT CGT CTC GGG TTT AGA ACA CTG TTT TGA TCA

FIG. 6B

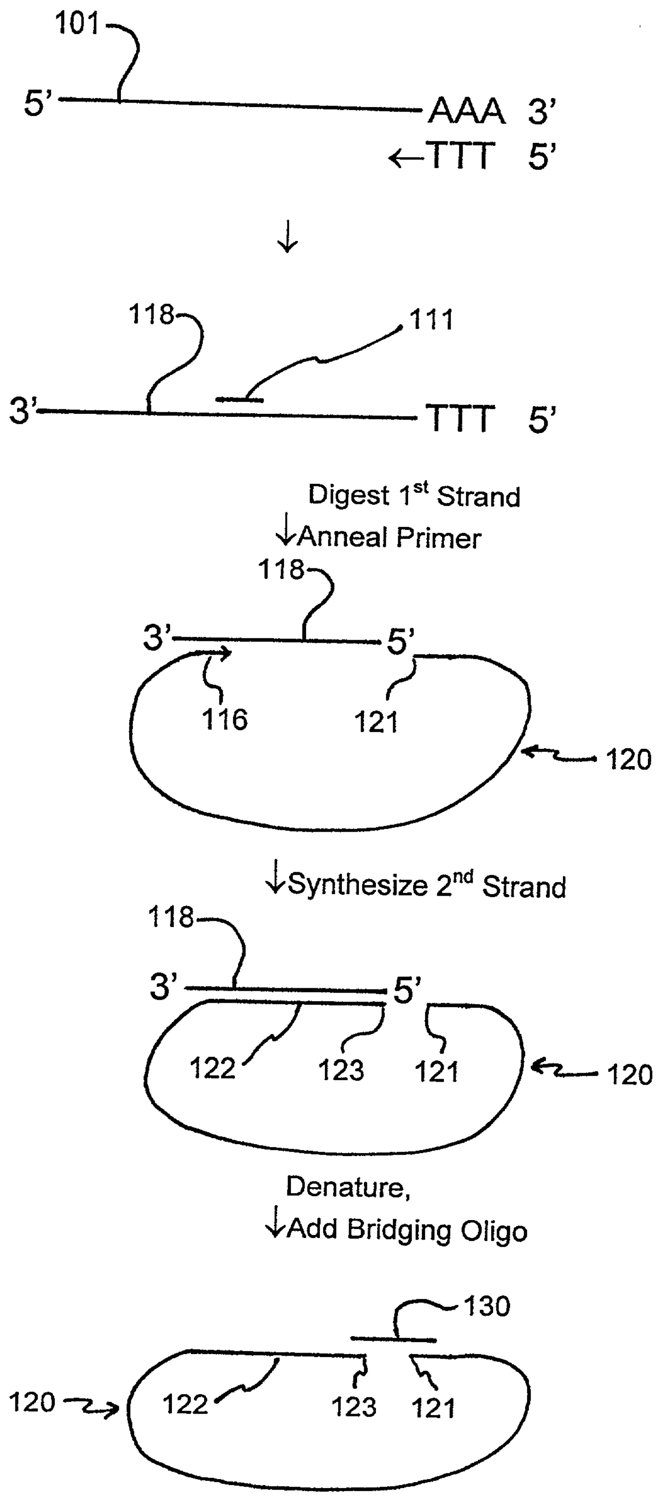
101
5'
AAA 3'
←TTT 5'
118
111
3'
TTT 5'
Digest 1st Strand
Anneal Primer
118
3'
5'
116
121
120
Synthesize 2nd Strand
118
3'
5'
122
123
121
120
Denature,
Add Bridging Oligo
130
120
122
123
121

Fig. 7